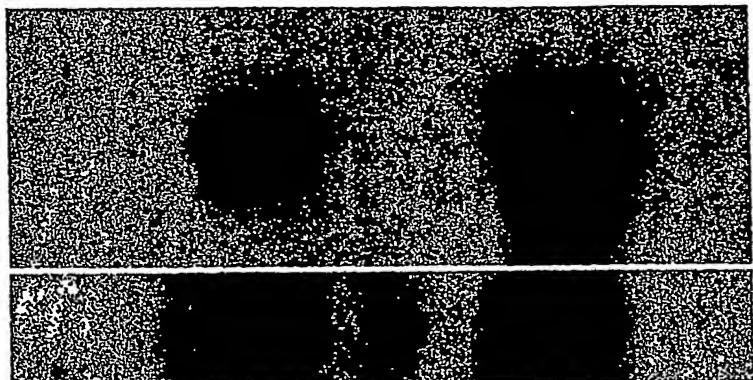
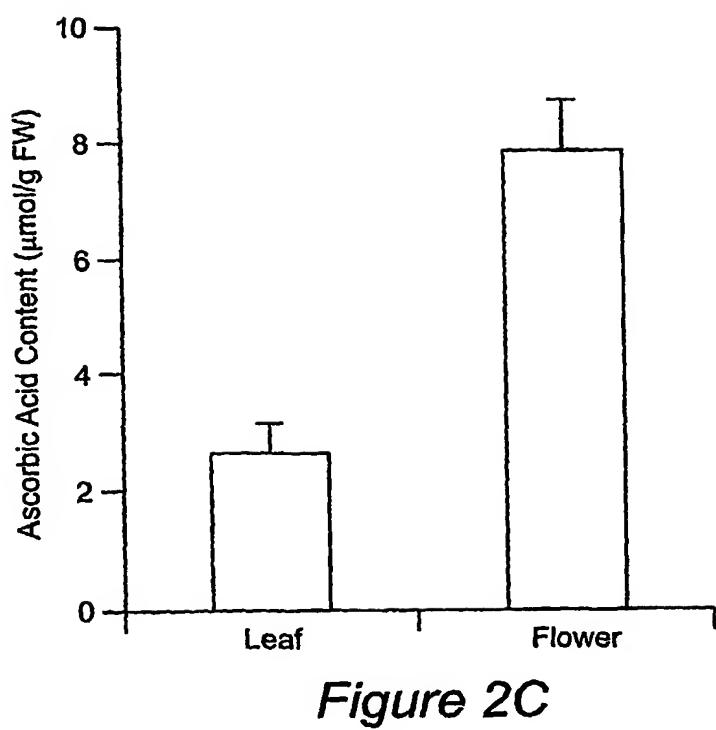


Figure 1

2/5

*Figure 2A**Figure 2B**Figure 2C*

3/5

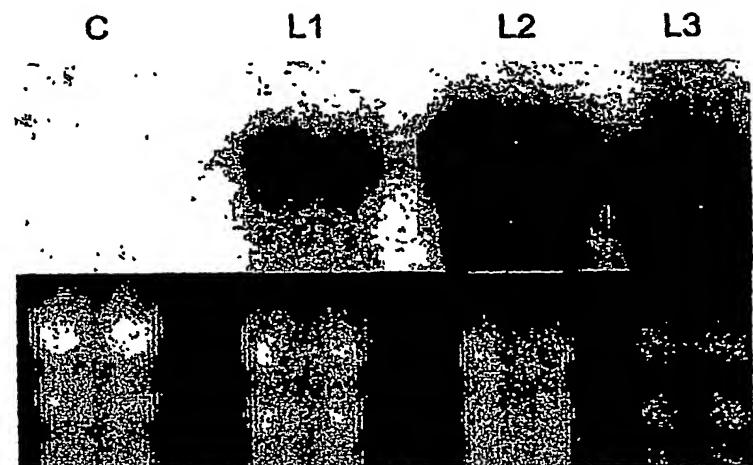


Figure 3B

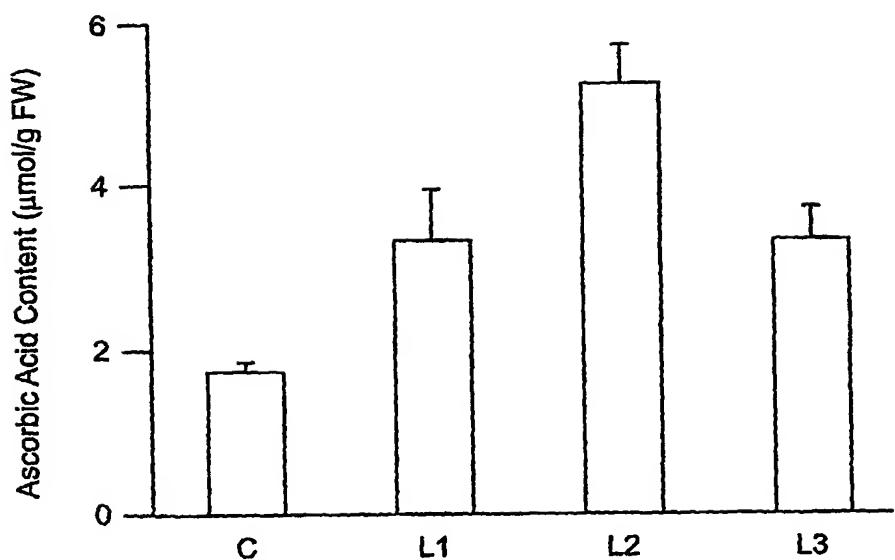


Figure 3C

SEQ ID NO:3

1	ATGACGATCT	CTGTTGAGAA	GCCGATTTTT	GAAGAAGAGG	TTTCTGCATT
51	CGAGAAGAGT	GGGGACAATA	TCGGAGAGTT	GAAATTGGAC	GGAGGATTTT
101	CGATGCCGAA	AATGGACACC	AATGACGACG	AAGCTTTTT	GGCTCCTGAG
151	ATGAATGCAT	TTGGCCGCCA	ATTCAGGGAC	TACGATGTTG	ACAGTGAGAG
201	GCAAAAGGGC	GTCGAAGAGT	TTTACAGATT	ACGACACATC	AACCAAACGT
251	TCGACTTTGT	GAAAAAGATG	AGGGCTGAAT	ATGGAAAATT	AGATAAAATG
301	GTGATGAGCA	TTTGGGAATG	TTGTGAGCTT	CTCAATGAGG	TTGTGATGA
351	GAGTGATCCA	GATCTTGACG	AGCCCCAGAT	TCAGCATTG	CTTCAATCTG
401	CCGAAGCCAT	CCGCAAAGAT	TACCCTAATG	AAGATTGGCT	TCATCTGACC
451	GCTCTTATCC	ATGATCTTGG	GAAAGTTATT	ACTCTTCCAC	AATTGGGAGG
501	ACTTCCTCAA	TGGGCTGTTG	TTGGTGACAC	ATTCCCTGTT	GGATGTGCAT
551	TTGATGAATC	TAACGTACAT	CACAAGTACT	TTGTGGAAAA	CCCAGATTTT
601	CACAACGAAA	CCTACAAACAC	AAAAATGGG	ATTTACTCTG	AAGGGTGTGG
651	ATTAAACAAAT	GTCATGATGT	CTTGGGGCCA	TGACGACTAC	ATGTACCTGG
701	TGGCTAAAGA	AAACGGAAGT	ACCTTGCCGT	CGGCTGGACA	GTTCATCATA
751	AGATACCACT	CCTTTACCC	TTTGCACACG	GCTGGAGAAT	ACACCCATCT
801	TATGAACGAG	GAAGACAAAGG	AGAATCTGAA	CTGGCTACAC	GTTCATCACA
851	AGTACGACTT	GTACAGTAAG	AGCAAAAGTTC	ACGTTGATGT	GGAGAAGGTC
901	GAGCCTTACT	ACATGTCTCT	TATCAAGAAA	TATTCCCGG	AAAACTTGAG
951	GTGG				

Figure 4

SEQ ID NO:4

1	MTISVEKPIF	EEEVSAFEKS	GDNIGELKLD	GGFSMPKMDT	40
41	NDDEAFLAPE	MNAFGRQFRD	YDVESERQKG	VEEFYRLRHI	80
81	NQTVDFVKKM	RAEYGKLDKM	VMSIWECCEL	LNEVVDESDP	120
121	DLDEPQIQHL	LQSAEAIRKD	YPNEDWLHLT	ALIHDILGKVI	160
161	TLPQFGGLPQ	WAVVGDTFPV	GCAFDESNVH	HKYFVENPDF	200
201	HNETYNTKNG	IYSEGCGLNN	VMMMSWGHDDY	MYLVAKENG	240
241	TLPSAGQFII	RYHSFYPLHT	AGEYTHLMNE	EDKENLKWLH	280
281	VFNKYDLYSK	SKVHVDVEKV	EPYYMSLIKK	YFPENLRW	318

*Figure 5*